PCT09

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RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/09/869,136   TIME: 13:24:46

Input Set : A:\39118.app
Output Set: N:\CRF3\01182002\I869136.raw

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 3 <110> APPLICANT: FRASER, JOHN DAVID
 4         PROFT, THOMAS
 6 <120> TITLE OF INVENTION: SUPERANTIGENS
 8 <130> FILE REFERENCE: 3911-8
10 <140> CURRENT APPLICATION NUMBER: 09/869,136
11 <141> CURRENT FILING DATE: 2001-07-20
13 <150> PRIOR APPLICATION NUMBER: PCT/NZ99/00228
14 <151> PRIOR FILING DATE: 1999-12-24
16 <150> PRIOR APPLICATION NUMBER: NZ 333589
17 <151> PRIOR FILING DATE: 1998-12-24
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn Ver. 2.1
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29 <221> NAME/KEY: CDS
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35  1               5                  10                  15
37 ata att tct cgt cct gtg ttt gga tta gaa gta gat aat aat tcc ctt    96
38 Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu
39              20                  25                  30
41 cta agg aat atc tat agt acg att gta tat gaa tat tca gat ata gta   144
42 Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val
43              35                  40                  45
45 att gat ttt aaa acc agt cat aac tta gtg act aag aaa ctt gat gtt   192
46 Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val
47      50                  55                  60
49 aga gat gct aga gat ttc ttt att aac tcc gaa atg gac gaa tat gca   240
50 Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala
51  65                  70                  75                  80
53 gcc aat gat ttt aaa act gga gat aaa ata gct gtg ttc tcc gtc cca   288
54 Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro
55                  85                  90                  95
57 ttt gat tgg aac tat tta tca aaa gga aaa gtc aca gca tat acc tat   336
58 Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr
59                 100                 105                 110
61 ggt gga ata aca ccc tac caa aaa act tca ata cct aaa aat atc cct   384
62 Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro
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66 Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu
67      130                 135                 140
69 ata tca act aac aaa aca aca gtt aca gct caa gaa att gat cta aag   480
70 Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys
71 145                 150                 155                 160
73 gtt aga aaa ttt tta ata gca caa cat caa tta tat tct tct ggt tct   528
74 Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser
75              165                 170                 175
77 agc tac aaa agt ggt aga ctg gtt ttt cat aca aat gat aat tca gat   576
78 Ser Tyr Lys Ser Gly Arg Leu Val Phe His Thr Asn Asp Asn Ser Asp
79              180                 185                 190
81 aaa tat tct ttc gat ctt ttc tat gta gga tat aga gat aaa gaa agt   624
82 Lys Tyr Ser Phe Asp Leu Phe Tyr Val Gly Tyr Arg Asp Lys Glu Ser
83          195                 200                 205
85 atc ttt aaa gta tac aaa gac aat aaa tct ttc aat ata gat aaa att   672
86 Ile Phe Lys Val Tyr Lys Asp Asn Lys Ser Phe Asn Ile Asp Lys Ile
87      210                 215                 220
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95 <211> LENGTH: 233
96 <212> TYPE: PRT
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99 <400> SEQUENCE: 2
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103 Ile Ile Ser Arg Pro Val Phe Gly Leu Glu Val Asp Asn Asn Ser Leu
104              20                 25                  30
106 Leu Arg Asn Ile Tyr Ser Thr Ile Val Tyr Glu Tyr Ser Asp Ile Val
107          35                 40                  45
109 Ile Asp Phe Lys Thr Ser His Asn Leu Val Thr Lys Lys Leu Asp Val
110      50                 55                  60
112 Arg Asp Ala Arg Asp Phe Phe Ile Asn Ser Glu Met Asp Glu Tyr Ala
113 65                 70                 75                  80
115 Ala Asn Asp Phe Lys Thr Gly Asp Lys Ile Ala Val Phe Ser Val Pro
116              85                 90                  95
118 Phe Asp Trp Asn Tyr Leu Ser Lys Gly Lys Val Thr Ala Tyr Thr Tyr
119              100                 105                 110
121 Gly Gly Ile Thr Pro Tyr Gln Lys Thr Ser Ile Pro Lys Asn Ile Pro
122          115                 120                 125
124 Val Asn Leu Trp Ile Asn Gly Lys Gln Ile Ser Val Pro Tyr Asn Glu
125      130                 135                 140
127 Ile Ser Thr Asn Lys Thr Thr Val Thr Ala Gln Glu Ile Asp Leu Lys
128 145                 150                 155                 160
130 Val Arg Lys Phe Leu Ile Ala Gln His Gln Leu Tyr Ser Ser Gly Ser
131              165                 170                 175
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137         195                 200                 205
139 Ile Phe Lys Val Tyr Lys Asp Asn Lys Ser Phe Asn Ile Asp Lys Ile
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153 <221> NAME/KEY: CDS
154 <222> LOCATION: (1)..(702)
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159   1                 5                 10                 15
161 tat gga agt caa tta gct tat gca gat gaa aat tta aaa gat tta aaa    96
162 Tyr Gly Ser Gln Leu Ala Tyr Ala Asp Glu Asn Leu Lys Asp Leu Lys
163             20                 25                 30
165 aga agt tta aga ttt gcc tat aat att acc cca tgc gat tat gaa aat   144
166 Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn
167         35                 40                 45
169 gta gaa att gca ttt gtt act aca aat agc ata cat att aat act aaa   192
170 Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys
171     50                 55                 60
173 caa aaa aga tcg gaa tgt att ctt tat gtt gat tct att gta tct tta   240
174 Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu
175 65                 70                 75                 80
177 ggc att act gat cag ttt ata aaa ggg gat aag gtc gat gtt ttt ggt   288
178 Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly
179             85                 90                 95
181 ctc cct tat aat ttt tcc cca cct tat gta gat aat att tat ggt ggt   336
182 Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly
183         100                 105                 110
185 att gta aaa cat tcg aat caa gga aat aaa tca tta cag ttt gta gga   384
186 Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly
187         115                 120                 125
189 att tta aat caa gat ggg aaa gaa act tat ttg ccc tct gag gct gtt   432
190 Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val
191     130                 135                 140
193 cgc ata aaa aag aaa cag ttt act tta cag gaa ttt gat ttt aaa ata   480
194 Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile
195 145                 150                 155                 160
197 aga aaa ttt cta atg gaa aaa tac aat atc tat gat tcg gaa tcg cgt   528
198 Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg
199             165                 170                 175
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201 tat aca tcg ggg agc ctt ttc ctt gct act aaa gat agt aaa cat tat   576
202 Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr
203             180             185             190
205 gaa gtt gat tta ttt aat aag gat gat aag ctt tta agt cga gac agt   624
206 Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser
207         195             200             205
209 ttc ttt aaa agg tat aaa gat aat aag att ttt aat agt gaa gaa att   672
210 Phe Phe Lys Arg Tyr Lys Asp Asn Lys Ile Phe Asn Ser Glu Glu Ile
211     210             215             220
213 agt cat ttt gat atc tac tta aaa acg cac tag                       705
214 Ser His Phe Asp Ile Tyr Leu Lys Thr His
215 225             230
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219 <211> LENGTH: 234
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221 <213> ORGANISM: Streptococcus pyogenes
223 <400> SEQUENCE: 4
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228             20              25              30
230 Arg Ser Leu Arg Phe Ala Tyr Asn Ile Thr Pro Cys Asp Tyr Glu Asn
231         35              40              45
233 Val Glu Ile Ala Phe Val Thr Thr Asn Ser Ile His Ile Asn Thr Lys
234     50              55              60
236 Gln Lys Arg Ser Glu Cys Ile Leu Tyr Val Asp Ser Ile Val Ser Leu
237 65              70              75                  80
239 Gly Ile Thr Asp Gln Phe Ile Lys Gly Asp Lys Val Asp Val Phe Gly
240             85              90                  95
242 Leu Pro Tyr Asn Phe Ser Pro Pro Tyr Val Asp Asn Ile Tyr Gly Gly
243             100             105             110
245 Ile Val Lys His Ser Asn Gln Gly Asn Lys Ser Leu Gln Phe Val Gly
246         115             120             125
248 Ile Leu Asn Gln Asp Gly Lys Glu Thr Tyr Leu Pro Ser Glu Ala Val
249     130             135             140
251 Arg Ile Lys Lys Lys Gln Phe Thr Leu Gln Glu Phe Asp Phe Lys Ile
252 145             150             155                 160
254 Arg Lys Phe Leu Met Glu Lys Tyr Asn Ile Tyr Asp Ser Glu Ser Arg
255             165             170             175
257 Tyr Thr Ser Gly Ser Leu Phe Leu Ala Thr Lys Asp Ser Lys His Tyr
258             180             185             190
260 Glu Val Asp Leu Phe Asn Lys Asp Asp Lys Leu Leu Ser Arg Asp Ser
261         195             200             205
263 Phe Phe Lys Arg Tyr Lys Asp Asn Lys Ile Phe Asn Ser Glu Glu Ile
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267 225             230
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277 <221> NAME/KEY: CDS
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285 atg att ata tgt ttg tca ttt ctt tta tat tcc aat gtt gtt caa gca    96
286 Met Ile Ile Cys Leu Ser Phe Leu Leu Tyr Ser Asn Val Val Gln Ala
287                20                  25                  30
289 aat tct tat aat aca acc aat aga cat aat cta gaa tcg ctt tat aag   144
290 Asn Ser Tyr Asn Thr Thr Asn Arg His Asn Leu Glu Ser Leu Tyr Lys
291                35                  40                  45
293 cat gat tct aac ttg att gaa gcc gat agt ata aaa aat tct cca gat   192
294 His Asp Ser Asn Leu Ile Glu Ala Asp Ser Ile Lys Asn Ser Pro Asp
295        50                  55                  60
297 att gta aca agc cat atg ttg aaa tat agt gtc aag gat aaa aat ttg   240
298 Ile Val Thr Ser His Met Leu Lys Tyr Ser Val Lys Asp Lys Asn Leu
299  65                  70                  75                  80
301 tca gtt ttt ttt gag aaa gat tgg ata tca cag gaa ttc aaa gat aaa   288
302 Ser Val Phe Phe Glu Lys Asp Trp Ile Ser Gln Glu Phe Lys Asp Lys
303                85                  90                  95
305 gaa gta gat att tat gct cta tct gca caa gag gtt tgt gaa tgt cca   336
306 Glu Val Asp Ile Tyr Ala Leu Ser Ala Gln Glu Val Cys Glu Cys Pro
307               100                 105                 110
309 ggg aaa agg tat gaa gcg ttt ggt gga att aca tta act aat tca gaa   384
310 Gly Lys Arg Tyr Glu Ala Phe Gly Gly Ile Thr Leu Thr Asn Ser Glu
311               115                 120                 125
313 aaa aaa gaa att aaa gtt cct gta aac gtg tgg gat aaa agt aaa caa   432
314 Lys Lys Glu Ile Lys Val Pro Val Asn Val Trp Asp Lys Ser Lys Gln
315        130                 135                 140
317 cag ccg cct atg ttt att aca gtc aat aaa ccg aaa gta acc gct cag   480
318 Gln Pro Pro Met Phe Ile Thr Val Asn Lys Pro Lys Val Thr Ala Gln
319 145                 150                 155                 160
321 gaa gtg gat ata aaa gtt aga aag tta ttg att aag aaa tac gat atc   528
322 Glu Val Asp Ile Lys Val Arg Lys Leu Leu Ile Lys Lys Tyr Asp Ile
323               165                 170                 175
325 tat aat aac cgg gaa caa aaa tac tct aaa gga act gtt acc tta gat   576
326 Tyr Asn Asn Arg Glu Gln Lys Tyr Ser Lys Gly Thr Val Thr Leu Asp
327               180                 185                 190
329 tta aat tca ggt aaa gat att gtt ttt gat ttg tat tat ttt ggc aat   624
330 Leu Asn Ser Gly Lys Asp Ile Val Phe Asp Leu Tyr Tyr Phe Gly Asn
331               195                 200                 205
333 gga gac ttt aat agc atg cta aaa ata tat tcc aat aac gag aga ata   672
334 Gly Asp Phe Asn Ser Met Leu Lys Ile Tyr Ser Asn Asn Glu Arg Ile
335        210                 215                 220
337 gac tca act caa ttt cat gta gat gtg tca atc agc taa               711
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